

This Listing of Claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for diagnosing a precancerous lesion or a cancer in a mammal, comprising:

detecting and measuring ~~the WIP1~~ gene copy number of a WIP1 gene having a nucleotide sequence homology of at least 70% sequence identity to SEQ ID NO:1 or SEQ ID NO:3 in a biological sample ~~subject~~ from a region of the mammal that is suspected to be precancerous or cancerous, thereby generating data for a test gene copy number; and

comparing the test gene copy number to data for a control gene copy number, wherein an amplification of the gene in the biological sample ~~subject~~ relative to the control indicates the presence of a precancerous lesion or cancer in the mammal.

2. (Currently Amended) The method according to claim 1, wherein the biological sample ~~subject~~ is selected from the group consisting of breast tissue, lung tissue, prostate tissue, ovarian tissue, and colon tissue.

3. (Original) The method according to claim 1, wherein the data is stored in an electronic or a paper format, wherein the electronic format is selected from the group consisting of electronic mail, disk, compact disk (CD), digital versatile disk (DVD), memory card, memory chip, ROM or RAM, magnetic optical disk, tape, video, video clip, microfilm, internet, shared network, shared server; wherein the data is displayed, transmitted or analyzed via physical transfer, electronic transmission, video display, or telecommunication; wherein the data is compared and compiled at the site of sampling specimens or at a location where the data is transmitted.

Claims 4-38 (Cancelled)

39. (NEW) The method according to claim 1 wherein said WIP1 gene associated with

said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 90% sequence identity to SEQ ID NO:1 or SEQ ID NO:3.

40. (NEW) The method according to claim 2 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 90% sequence identity to SEQ ID NO:1 or SEQ ID NO:3.

41. (NEW) The method according to claim 3 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 90% sequence identity to SEQ ID NO:1 or SEQ ID NO:3.

42. (NEW) The method according to claim 1 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 95% sequence identity to SEQ ID NO:1 or SEQ ID NO:3.

43. (NEW) The method according to claim 2 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 95% sequence identity to SEQ ID NO:1 or SEQ ID NO:3.

44. (NEW) The method according to claim 3 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 95% sequence identity to SEQ ID NO:1 or SEQ ID NO:3.

45. (NEW) The method according to claim 1 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3.

46. (NEW) The method according to claim 2 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence of SEQ ID

NO:1 or SEQ ID NO:3.

47. (NEW) The method according to claim 3 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3.

48. (NEW) The method according to claim 1 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 90% sequence identity to SEQ ID NO:1.

49. (NEW) The method according to claim 2 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 90% sequence identity to SEQ ID NO:1.

50. (NEW) The method according to claim 3 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 90% sequence identity to SEQ ID NO:1.

51. (NEW) The method according to claim 1 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 95% sequence identity to SEQ ID NO:1.

52. (NEW) The method according to claim 2 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 95% sequence identity to SEQ ID NO:1.

53. (NEW) The method according to claim 3 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence homology of at least 95% sequence identity to SEQ ID NO:1.

54. (NEW) The method according to claim 1 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence of SEQ ID NO:1.

55. (NEW) The method according to claim 2 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence of SEQ ID NO:1.

56. (NEW) The method according to claim 3 wherein said WIP1 gene associated with said detecting and measuring of said gene copy number has a nucleotide sequence of SEQ ID NO:1.